

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LI, Yi
- (ii) TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
 - (B) STREET: 6 Becker Farm Road
 - (C) CITY: Roseland
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 07068-1739
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WordPerfect 5.1, Dos Text File
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/466,343
 - (B) FILING DATE: 6 JUN 1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: MULLINS, J.G.
 - (B) REGISTRATION NUMBER: 33,073
 - (C) REFERENCE/DOCKET NUMBER: 325800-449
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 201-994-1700
 - (B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 1414 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGAGATGGT GCTTTCATGA ATTCCCCCAA CAAGAGCCAA GCTCTCCATC TAGTGGACAG 60

GGAAGCTAGC AGCAAACCTT CCCTTCACTA CGAAACTTCA TTGCTTGGCC CAAAAGAGAG 120

TTAATTCAAT GTAGACATCT ATGTAGGCAA TTAAAAACCT ATTGATGTAT AAAACAGTTT 180

GCATTCATGG AGGGCAACTA AATACATTCT AGGACTTTAT AAAAGATCAC TTTTATTTA 240

TGCACAGGGT GGAACAAG ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC 291
Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp
5 10

ATC AAT TAT TAT ACA TCG GAG CCC TGC CCA AAA ATC AAT GTG AAG CAA 339
Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln
15 20 25

ATC GCA GCC CGC CTC CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT 387
Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe
30 35 40

GGT TTT GTG GGC AAC ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC CAA 435
Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln
45 50 55

AGG CTG GAG AGC ATG ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT 483
Arg Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
60 65 70 75

GAC CTG TTT TTC CTT CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC 531
Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala
80 85 90

GCC CAG TGG GAC TTT GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC 579
Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly Leu Tyr
95 100 105
102 now should be Gln(P)

TAT TTT ATA GGC TTC TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA 627
Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln Leu Leu Thr
110 115 120
ATC = Leu

ATC GAT AGG TAC CTG GCT ATC GTC CAT GCT GTG TTT GCT TTA AAA GCC 675
Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala
125 130 135

AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG 723
Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Val Val
140 145 150 155

GCT GTG TTT GCG TCT CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA 771
Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys
160 165 170

GAA GGT CTT CAT TAC ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT 819
Glu Gly Leu His Tyr Thr cys Ser Ser His Phe Pro Tyr Ser Gln Tyr
175 180 185

CAA TTC TGG AAG AAT TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG 867
Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu
190 195 200

GTC CTG CCG CTG CTT GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA 915
Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys
205 210 215

ACT CTG CTT CGG TGT CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG 963
Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg
220 225 230 235

CTT ATC TTC ACC ATC ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC 1011
 Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr
 240 245 250
 AAC ATT GTC CTT CTC CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT 1059
 Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn
 255 260 265
 AAT TGC AGT AGC TCT AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG 1107
 Asn Cys Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu
 270 275 280
 ACT CTT GGG ATG ACG CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT 1155
 Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe
 285 290 295
 GTC GGG GAG AAG TTC AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC 1203
 Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His
 300 305 310 315
 ATT GCC AAA CGC TTC TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT 1251
 Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala
 320 325 330
 CCC GAG CGA GCA AGC TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA 1299
 Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu
 335 340 345
 ATA TCT GTG GGC TTG TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG 1354
 Ile Ser Val Gly Leu
 350
 TGCACATGGC TTAGTTTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGAA GAGGTCTTTT 1414

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 352 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr
 5 10 15
 Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln Ile Ala Ala
 20 25 30
 Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe
 35 40 45
 Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln Arg
 50 55 60
 Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
 65 70 75

Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala
 80 85 90
 Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly
 95 100 105
 Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln
 110 115 120
 Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
 125 130 135
 Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val
 140 145 150
 Ile Thr Trp Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile
 155 160 165
 Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr cys Ser Ser
 170 175 180
 His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr
 185 190 195
 Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu Val Met
 200 205 210
 Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg
 215 220 225
 Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
 230 235 240
 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu
 245 250 255
 Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser
 260 265 270
 Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu
 275 280 285
 Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val
 290 295 300
 Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His
 305 310 315
 Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu
 320 325 330
 Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu
 335 340 345

Gln Glu Ile Ser Val Gly Leu
350

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 30 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGAATTCCT CCATGGATTA TCAAGTGTC A 30

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 29 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGAAGCTTC GTCACAAGCC CACAGATAT 29

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 34 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCAAGCTT GCCACCATGG ATTATCAAGT GTCA 34

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 61 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCACAAGCCC ACAGATATTT 60

C

61

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 30 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGGATCCCT CCATGGATTA TCAAGTGTC

30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 29 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGGATCCCG CTCACAAGCC CACAGATAT

29

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
5 10 15

His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro

	20	25	30
Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu	35	40	45
Val Val Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr	50	55	60
Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu	65	70	75
Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val	80	85	90
Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile	95	100	105
Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp	110	115	120
Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg	125	130	135
Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Leu Val	140	145	150
Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys Gln	155	160	165
Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly	170	175	180
Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val	185	190	195
Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys	200	205	210
Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val	215	220	225
Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr	230	235	240
Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe	245	250	255
Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr	260	265	270
Gln Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro	275	280	285

Ile	Ile	Tyr	Ala	Phe	Val	Gly	Glu	Lys	Phe	Arg	Ser	Leu	Phe	His
				290					295					300
Ile	Ala	Leu	Gly	Cys	Arg	Ile	Ala	Pro	Leu	Gln	Lys	Pro	Val	Cys
				305					310					315
Gly	Gly	Pro	Gly	Val	Arg	Pro	Gly	Lys	Asn	Val	Lys	Val	Thr	Thr
				320					325					330
Gln	Gly	Leu	Leu	Asp	Gly	Arg	Gly	Lys	Gly	Lys	Ser	Ile	Gly	
				335					340					

D'
level.